RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/828,831_

Source: _1PWO_

Date Processed by STIC: _09-28-2005_

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RAW SEQUENCE LISTING   DATE: 09/28/2005
PATENT APPLICATION: **US/10/828,831**   TIME: 07:54:40

Input Set : **N:\Crf3\RULE60\10828831.raw.txt**
Output Set: **N:\CRF4\09282005\J828831.raw**

```
  1 <110> APPLICANT: EVANS, RONALD M.
  2        NO, DAVID
  3        SAEZ, ENRIQUE
  4 <120> TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN
  5        MAMMALIAN SYSTEMS, AND PRODUCTS REALTED THERETO
  6 <130> FILE REFERENCE: SALK1520-2
  7 <140> CURRENT APPLICATION NUMBER: US/10/828,831
  8 <141> CURRENT FILING DATE: 2004-04-20
  9 <150> PRIOR APPLICATION NUMBER: US/09/042,488
 10 <151> PRIOR FILING DATE: 1998-03-16
 11 <150> PRIOR APPLICATION NUMBER: 08/974,530
 12 <151> PRIOR FILING DATE: 1997-11-19
 13 <150> PRIOR APPLICATION NUMBER: 08/628,830
 14 <151> PRIOR FILING DATE: 1996-04-05
 15 <160> NUMBER OF SEQ ID NOS: 18
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 71
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Artificial Sequence
 22 <220> FEATURE:
 23 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
 24        peptide sequence
W--> 25 <221> NAME/KEY: MOD_RES
 26 <222> LOCATION: (2)..(3)
 27 <223> OTHER INFORMATION: Any amino acid
W--> 28 <221> MOD_RES
 29 <222> LOCATION: (5)..(6)
 30 <223> OTHER INFORMATION: Any amino acid
W--> 31 <221> MOD_RES
 32 <222> LOCATION: (8)
 33 <223> OTHER INFORMATION: Any amino acid
W--> 34 <221> MOD_RES
 35 <222> LOCATION: (10)
 36 <223> OTHER INFORMATION: Any amino acid
W--> 37 <221> MOD_RES
 38 <222> LOCATION: (12)
 39 <223> OTHER INFORMATION: Any amino acid
W--> 40 <221> MOD_RES
 41 <222> LOCATION: (14)..(17)
 42 <223> OTHER INFORMATION: Any amino acid
W--> 43 <221> MOD_RES
 44 <222> LOCATION: (19)..(20)
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        45 <223> OTHER INFORMATION: Any amino acid
W--> 46 <221> MOD_RES
        47 <222> LOCATION: (23)
        48 <223> OTHER INFORMATION: Any amino acid
W--> 49 <221> MOD_RES
        50 <222> LOCATION: (26)
        51 <223> OTHER INFORMATION: Any amino acid
W--> 52 <221> MOD_RES
        53 <222> LOCATION: (28)..(38)
        54 <223> OTHER INFORMATION: Any amino acid
W--> 55 <221> MOD_RES
        56 <222> LOCATION: (40)..(47)
        57 <223> OTHER INFORMATION: Any amino acid
W--> 58 <221> MOD_RES
        59 <222> LOCATION: (49)..(51)
        60 <223> OTHER INFORMATION: Any amino acid
W--> 61 <221> MOD_RES
        62 <222> LOCATION: (53)..(54)
        63 <223> OTHER INFORMATION: Any amino acid
W--> 64 <221> MOD_RES
        65 <222> LOCATION: (56)..(57)
        66 <223> OTHER INFORMATION: Any amino acid
W--> 67 <221> MOD_RES
        68 <222> LOCATION: (59)..(60)
        69 <223> OTHER INFORMATION: Any amino acid
W--> 70 <221> MOD_RES
        71 <222> LOCATION: (63)..(64)
        72 <223> OTHER INFORMATION: Any amino acid
W--> 73 <221> MOD_RES
        74 <222> LOCATION: (67)..(69)
        75 <223> OTHER INFORMATION: Any amino acid
W--> 76 <400> 1
W--> 77      Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
        78      1               5                  10              Tyr      15
        79      Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
        80                      20                  25              30
        81      Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
        82                  35                  40                  45
        83      Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
        84          50                  55                  60
        85      Lys Cys Xaa Xaa Xaa Gly Met
        86      65                  70
        88 <210> SEQ ID NO: 2
        89 <211> LENGTH: 5
        90 <212> TYPE: PRT
        91 <213> ORGANISM: Artificial Sequence
        92 <220> FEATURE:
        93 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
        94      peptide
```

```
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              PATENT APPLICATION:  US/10/828,831    TIME: 07:54:40

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              Output Set: N:\CRF4\09282005\J828831.raw
```

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 95 <400> SEQUENCE: 2
 96       Glu Gly Cys Lys Gly
 97         1                 5
 99 <210> SEQ ID NO: 3
100 <211> LENGTH: 5
101 <212> TYPE: PRT
102 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
105       peptide
106 <400> SEQUENCE: 3
107       Gly Ser Cys Lys Val
108         1                 5
110 <210> SEQ ID NO: 4
111 <211> LENGTH: 2241
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Description of Artificial Sequence: Recombinant
116       VgEcR
```
W--> 117 `<221> NAME/KEY: CDS`
```
118 <222> LOCATION: (1)..(2238)
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W--> 119 `<400> 4`
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120       atg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac    48
121       Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
122         1                 5                  10                  15
123       ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat    96
124       Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
125                          20                  25                  30
126       ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc   144
127       Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
128                      35                  40                  45
129       cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt   192
130       His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
131              50                  55                  60
132       gag cag atg ttt acc gat gcc ctt gga att gac gag tac ggt ggg aag   240
133       Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
134          65                  70                  75                  80
135       ctt cta ggt acc tct aga agg ata tcg aat tct ata tct tca ggt cgc   288
136       Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
137                          85                  90                  95
138       gat gat ctc tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa   336
139       Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
140                         100                 105                 110
141       agc tgc gat gcg aag aag agc aag aag gga cct gcg cca cgg gtg caa   384
142       Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
143                     115                 120                 125
144       gag gag ctg tgc ctg gtt tgc ggc gac agg gcc tcc ggc tac cac tac   432
145       Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
```

```
146        130                  135                  140
147    aac gcc ctc acc tgt gga tcc tgc aag gtg ttc ttt cga cgc agc gtt   480
148    Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val
149    145                  150                  155                  160
150    acg aag agc gcc gtc tac tgc tgc aag ttc ggg cgc gcc tgc gaa atg   528
151    Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
152                       165                  170                  175
153    gac atg tac atg agg cga aag tgt cag gag tgc cgc ctg aaa aag tgc   576
154    Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
155                       180                  185                  190
156    ctg gcc gtg ggt atg cgg ccg gaa tgc gtc gtc ccg gag aac caa tgt   624
157    Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
158                  195                  200                  205
159    gcg atg aag cgg cgc gaa aag aag gcc cag aag gag aag gac aaa atg   672
160    Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
161         210                  215                  220
162    acc act tcg ccg agc tct cag cat ggc ggc aat ggc agc ttg gcc tct   720
163    Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
164    225                  230                  235                  240
165    ggt ggc ggc caa gac ttt gtt aag aag gag att ctt gac ctt atg aca   768
166    Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
167                       245                  250                  255
168    tgc gag ccg ccc cag cat gcc act att ccg cta cta cct gat gaa ata   816
169    Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
170                       260                  265                  270
171    ttg gcc aag tgt caa gcg cgc aat ata cct tcc tta acg tac aat cag   864
172    Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
173                  275                  280                  285
174    ttg gcc gtt ata tac aag tta att tgg tac cag gat ggc tat gag cag   912
175    Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
176         290                  295                  300
177    cca tct gaa gag gat ctc agg cgt ata atg agt caa ccc gat gag aac   960
178    Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
179    305                  310                  315                  320
180    gag agc caa acg gac gtc agc ttt cgg cat ata acc gag ata acc ata   1008
181    Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
182                       325                  330                  335
183    ctc acg gtc cag ttg att gtt gag ttt gct aaa ggt cta cca gcg ttt   1056
184    Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
185                       340                  345                  350
186    aca aag ata ccc cag gag gac cag atc acg tta cta aag gcc tgc tcg   1104
187    Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
188                  355                  360                  365
189    tcg gag gtg atg atg ctg cgt atg gca cga cgc tat gac cac agc tcg   1152
190    Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
191         370                  375                  380
192    gac tca ata ttc ttc gcg aat aat aga tca tat acg cgg gat tct tac   1200
193    Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
194    385                  390                  395                  400
```

```
195        aaa atg gcc gga atg gct gat aac att gaa gac ctg ctg cat ttc tgc        1248
196        Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
197                    405                     410                     415
198        cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc        1296
199        Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
200                    420                     425                     430
201        act gcc att gtg atc ttc tcg gac cgg ccg ggc ctg gag aag gcc caa        1344
202        Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
203                    435                     440                     445
204        cta gtc gaa gcg atc cag agc tac tac atc gac acg cta cgc att tat        1392
205        Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
206                    450                     455                     460
207        ata ctc aac cgc cac tgc ggc gac tca atg agc ctc gtc ttc tac gca        1440
208        Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
209        465                     470                     475                     480
210        aag ctg ctc tcg atc ctc acc gag ctg cgt acg ctg ggc aac cag aac        1488
211        Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
212                    485                     490                     495
213        gcc gag atg tgt ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag        1536
214        Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
215                    500                     505                     510
216        ttc ctc gag gag atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag        1584
217        Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
218                    515                     520                     525
219        tcg cac ctt cag att acc cag gag gag aac gag cgt ctc gag cgg gct        1632
220        Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
221        530                     535                     540
222        gag cgt atg cgg gca tcg gtt ggg ggc gcc att acc gcc ggc att gat        1680
223        Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
224        545                     550                     555                     560
225        tgc gac tct gcc tcc act tcg gcg gcg gca gcc gcg gcc cag cat cag        1728
226        Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
227                    565                     570                     575
228        cct cag cct cag ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat        1776
229        Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
230                    580                     585                     590
231        tcc cag cac cag aca cag ccg cag cta caa cct cag cta cca cct cag        1824
232        Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
233                    595                     600                     605
234        ctg caa ggt caa ctg caa ccc cag ctc caa cca cag ctt cag acg caa        1872
235        Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
236                    610                     615                     620
237        ctc cag cca cag att caa cca cag cca cag ctc ctt ccc gtc tcc gct        1920
238        Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
239        625                     630                     635                     640
240        ccc gtg ccc gcc tcc gta acc gca cct ggt tcc ttg tcc gcg gtc agt        1968
241        Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
242                    645                     650                     655
243        acg agc agc gaa tac atg ggc gga agt gcg gcc ata gga ccc atc acg        2016
```

```
              RAW SEQUENCE LISTING ERROR SUMMARY    DATE: 09/28/2005
              PATENT APPLICATION:  US/10/828,831    TIME: 07:54:41

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```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:1; Xaa Pos. 2,3,5,6,8,10,12,14,15,16,17,19,20,23,26,28,29,30,31,32,33
Seq#:1; Xaa Pos. 34,35,36,37,38,40,41,42,43,44,45,46,47,49,50,51,53,54,56
Seq#:1; Xaa Pos. 57,59,60,63,64,67,68,69
Seq#:10; N Pos. 4,5,7,8,9,10,11,14,15
Seq#:11; N Pos. 3,4,7,8,9,10,11,13,14
Seq#:12; N Pos. 7
Seq#:13; N Pos. 4,5,7,8,9,10,11,15,16
```

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

```
Seq#:1; Line(s) 4
Seq#:10; Line(s) 980
Seq#:11; Line(s) 1001
Seq#:13; Line(s) 1035
```

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Input Set : **N:\Crf3\RULE60\10828831.raw.txt**
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```
L:25 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:28 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:31 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:34 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:40 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:49 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:52 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:55 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:58 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:61 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:64 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:67 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:70 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:73 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:76 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
M:341 Repeated in SeqNo=1
L:117 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:119 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:372 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:374 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:627 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:629 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:975 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:978 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:983 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:986 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:996 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:999 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:1004 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:1007 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:1008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:1017 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1020 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:1030 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1033 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:1038 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:1041 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:1042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
```